



SEQUENCE LISTING

<110> Turner, Alex
Zambrowicz, Brian
Nehls, Michael
Freidrich, Glenn A.
Sands, Arthur T.

<120> NOVEL HUMAN GENES AND PROTEINS
ENCODED THEREBY

<130> 8535-0036-999

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1116

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(1113)

<400> 1

atg gga cat aaa gtg gtt gtc ttc gac att tct gtc atc aga gcc ttg	48
Met Gly His Lys Val Val Val Phe Asp Ile Ser Val Ile Arg Ala Leu	
1 5 10 15	

tgg gaa act cgt gtc aag aag cac aaa gct tgg cag aag aag gag gtg	96
Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val	
20 25 30	

gaa agg ctt gag aag agc gcc ttg gag aag ata aag gag gag tgg aac	144
Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Glu Trp Asn	
35 40 45	

ttt gtg gcc gaa tgc agg agg aag ggc atc ccc cag gct gta tac tgc	192
Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys	
50 55 60	

aag aat ggc ttc ata gac acc agc gtg cgg ctt ctg gac aag att gaa	240
Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Leu Asp Lys Ile Glu	
65 70 75 80	

agg aac act ctc aca agg cag agt tca ctt ccc aag gac aga ggc aaa	288
Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys	
85 90 95	

cgg agc agt gcg ttt gtg ttt gaa ctt tct ggg gag cac tgg acg gag	336
Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu	
100 105 110	

ctc cca gat tca ttg aag gag cag aca cac ctg aga gaa tgg tac ata	384
Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile	
115 120 125	
agc aat acc ttg att caa atc att cct aca tat att cag tta ttt caa	432
Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln	
130 135 140	
gcg atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca	480
Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro	
145 150 155 160	
gca gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc	528
Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe	
165 170 175	
aac tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta	576
Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu	
180 185 190	
gag aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt	624
Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe	
195 200 205	
gaa tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac	672
Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn	
210 215 220	
aag ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tcg aat ttg cag	720
Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln	
225 230 235 240	
tgg ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata	768
Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile	
245 250 255	
gac agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg	816
Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu	
260 265 270	
acc tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta	864
Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu	
275 280 285	
gtc gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac	912
Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp	
290 295 300	
tca tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat	960
Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp	
305 310 315 320	
aat gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat	1008
Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp	
325 330 335	

cgc	caa	cat	ttt	gat	aaa	gaa	gtt	atg	aaa	gcc	tat	att	gaa	gac	ctt	1056
Arg	Gln	His	Phe	Asp	Lys	Glu	Val	Met	Lys	Ala	Tyr	Ile	Glu	Asp	Leu	
			340					345					350			
aaa	gaa	aga	gaa	tct	gtt	ccc	agc	tat	acc	acc	aaa	gtg	tct	ttt	agc	1104
Lys	Glu	Arg	Glu	Ser	Val	Pro	Ser	Tyr	Thr	Thr	Lys	Val	Ser	Phe	Ser	
		355					360					365				
ctt	caa	ctt	tga													1116
Leu	Gln	Leu														
		370														

<210> 2
 <211> 371
 <212> PRT
 <213> Homo sapien

<400> 2																
Met	Gly	His	Lys	Val	Val	Val	Phe	Asp	Ile	Ser	Val	Ile	Arg	Ala	Leu	
1				5					10					15		
Trp	Glu	Thr	Arg	Val	Lys	Lys	His	Lys	Ala	Trp	Gln	Lys	Lys	Glu	Val	
			20					25					30			
Glu	Arg	Leu	Glu	Lys	Ser	Ala	Leu	Glu	Lys	Ile	Lys	Glu	Glu	Trp	Asn	
		35					40					45				
Phe	Val	Ala	Glu	Cys	Arg	Arg	Lys	Gly	Ile	Pro	Gln	Ala	Val	Tyr	Cys	
	50					55					60					
Lys	Asn	Gly	Phe	Ile	Asp	Thr	Ser	Val	Arg	Leu	Leu	Asp	Lys	Ile	Glu	
65					70					75				80		
Arg	Asn	Thr	Leu	Thr	Arg	Gln	Ser	Ser	Leu	Pro	Lys	Asp	Arg	Gly	Lys	
			85						90					95		
Arg	Ser	Ser	Ala	Phe	Val	Phe	Glu	Leu	Ser	Gly	Glu	His	Trp	Thr	Glu	
			100					105						110		
Leu	Pro	Asp	Ser	Leu	Lys	Glu	Gln	Thr	His	Leu	Arg	Glu	Trp	Tyr	Ile	
		115					120					125				
Ser	Asn	Thr	Leu	Ile	Gln	Ile	Ile	Pro	Thr	Tyr	Ile	Gln	Leu	Phe	Gln	
	130					135					140					
Ala	Met	Arg	Ile	Leu	Asp	Leu	Pro	Lys	Asn	Gln	Ile	Ser	His	Leu	Pro	
145					150					155				160		
Ala	Glu	Ile	Gly	Cys	Leu	Lys	Asn	Leu	Lys	Glu	Leu	Asn	Val	Gly	Phe	
			165					170						175		
Asn	Tyr	Leu	Lys	Ser	Ile	Pro	Pro	Glu	Leu	Gly	Asp	Cys	Glu	Asn	Leu	
		180						185					190			
Glu	Arg	Leu	Asp	Cys	Ser	Gly	Asn	Leu	Glu	Leu	Met	Glu	Leu	Pro	Phe	
		195					200					205				
Glu	Leu	Ser	Asn	Leu	Lys	Gln	Val	Thr	Phe	Val	Asp	Ile	Ser	Ala	Asn	
	210					215					220					
Lys	Phe	Ser	Ser	Val	Pro	Ile	Cys	Val	Leu	Arg	Met	Ser	Asn	Leu	Gln	
225					230					235				240		
Trp	Leu	Asp	Ile	Ser	Ser	Asn	Asn	Leu	Thr	Asp	Leu	Pro	Gln	Asp	Ile	
			245						250					255		
Asp	Arg	Leu	Glu	Glu	Leu	Gln	Ser	Phe	Leu	Leu	Tyr	Lys	Asn	Lys	Leu	
		260						265					270			
Thr	Tyr	Leu	Pro	Tyr	Ser	Met	Leu	Asn	Leu	Lys	Lys	Leu	Thr	Leu	Leu	
	275						280					285				
Val	Val	Ser	Gly	Asp	His	Leu	Val	Glu	Leu	Pro	Thr	Ala	Leu	Cys	Asp	
	290					295					300					

Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp
 305 310 315 320
 Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp
 325 330 335
 Arg Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu
 340 345 350
 Lys Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser
 355 360 365
 Leu Gln Leu
 370

<210> 3
 <211> 681
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(678)

<400> 3
 atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca gca 48
 Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala
 1 5 10 15
 gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc aac 96
 Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn
 20 25 30
 tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta gag 144
 Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu
 35 40 45
 aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt gaa 192
 Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
 50 55 60
 tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac aag 240
 Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
 65 70 75 80
 ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tcg aat ttg cag tgg 288
 Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
 85 90 95
 ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata gac 336
 Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
 100 105 110
 agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg acc 384
 Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
 115 120 125
 tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta gtc 432
 Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
 130 135 140

gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac tca	480
Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser	
145 150 155 160	
tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat aat	528
Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn	
165 170 175	
gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat cgc	576
Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg	
180 185 190	
caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt aaa	624
Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys	
195 200 205	
gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc ctt	672
Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu	
210 215 220	
caa ctt tga	681
Gln Leu	
225	

<210> 4
 <211> 226
 <212> PRT
 <213> Homo sapien

<400> 4

Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala	
1 5 10 15	
Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn	
20 25 30	
Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu	
35 40 45	
Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu	
50 55 60	
Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys	
65 70 75 80	
Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp	
85 90 95	
Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp	
100 105 110	
Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr	
115 120 125	
Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val	
130 135 140	
Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser	
145 150 155 160	
Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn	
165 170 175	
Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg	
180 185 190	
Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys	
195 200 205	

Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu
210 215 220
Gln Leu
225